

Freeform Search

Database:	US Pre-Grant Publication Full-Text Database	
	US Patents Full-Text Database	
	US OCR Full-Text Database	
	EPO Abstracts Database	
	JPO Abstracts Database	
	Derwent World Patents Index	
	IBM Technical Disclosure Bulletins	
Term:	<input type="text"/>	
Display:	<input type="text" value="10"/> Documents in <u>Display Format:</u>	<input type="text" value="CIT"/> Starting with Number <input type="text" value="1"/>
Generate:	<input type="radio"/> Hit List <input checked="" type="radio"/> Hit Count <input type="radio"/> Side by Side <input type="radio"/> Image	

Search History

DATE: Friday, July 15, 2005 [Printable Copy](#) [Create Case](#)

<u>Set</u> <u>Name</u> <u>Query</u> side by side	<u>Hit</u> <u>Count</u>	<u>Set</u> <u>Name</u> result set
<i>DB=PGPB,USPT; THES=ASSIGNEE; PLUR=YES; OP=OR</i>		
<u>L8</u> (triacylglycerol near5 lipase and immunoassay or tissue and endothel\$3 near10 lipase not Jaye.in. or Krawiec.in. or South.in. or Maugeais.in. or Rader.in. or Marchadier.in. or Amin.in. or Doan.in. and triacylglycerol near5 lipase)	23	<u>L8</u>
<u>L7</u> (triacylglycerol near5 lipase and immunoassay or tissue and endothel\$3 near10 lipase)	25	<u>L7</u>
<u>L6</u> (endothel\$3 near10 lipase)	125	<u>L6</u>
<u>L5</u> (triacylglycerol near5 lipase and immunoassay or tissue)	220	<u>L5</u>
<u>L4</u> (immunoassay or tissue)	315612	<u>L4</u>
<u>L3</u> (Jaye.in. or Krawiec.in. or South.in. or Maugeais.in. or Rader.in. or Marchadier.in. or Amin.in. or Doan.in. and triacylglycerol near5 lipase)	2	<u>L3</u>
<u>L2</u> (triacylglycerol near5 lipase)	340	<u>L2</u>
<u>L1</u> (Jaye.in. or Krawiec.in. or South.in. or Maugeais.in. or Rader.in. or Marchadier.in. or Amin.in. or Doan.in.)	2322	<u>L1</u>

END OF SEARCH HISTORY

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OM protein - protein search, using sw model

Run on: April 30, 2004, 08:03:07 ; Search time 46 Seconds
(without alignments)
3429.546 Million cell updates/sec

Title: US-09-277-401A-8
Perfect score: 2709
Sequence: 1 MSNSVPLLCFWSLCYCFAAG.....RKCRDGWRMKNETSPTVELP 500
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	1524.5	56.3	500	13	Q803Y3	Q803y3 brachydanio
2	1310.5	48.4	511	13	Q98UI3	Q98ui3 pagrus majo
3	1308.5	48.3	510	13	Q98UI2	Q98ui2 pagrus majo
4	1212.5	44.8	490	13	Q9PSV4	Q9psv4 gallus gall
5	1164	43.0	449	6	Q95KN9	Q95kn9 macaca fasc
6	1161	42.9	475	4	Q96FC4	Q96fc4 homo sapien

7	1155	42.6	474	11	Q8C562	Q8c562 mus musculu
8	1095.5	40.4	510	11	Q8VC44	Q8vc44 mus musculu
9	1089.5	40.2	510	11	Q80Z65	Q80z65 mus spretus
10	1088	40.2	514	13	Q7T359	Q7t359 brachydanio
11	1072	39.6	499	6	O46559	O46559 oryctolagus
12	1070.5	39.5	503	13	Q9W6Y2	Q9w6y2 oncorhynchus
13	890	32.9	332	6	O77644	O77644 pan troglod
14	748.5	27.6	330	13	Q92173	Q92173 brachydanio
15	604	22.3	200	11	Q8R4V8	Q8r4v8 cricetus
16	555	20.5	473	11	O70478	O70478 mus musculu
17	545.5	20.1	470	13	Q8QGWL	Q8qgw1 anguilla ja
18	536	19.8	467	4	Q8TAU2	Q8tau2 homo sapien
19	521.5	19.3	465	11	O88354	O88354 spermophilu
20	520.5	19.2	465	11	Q9QWF3	Q9qwf3 spermophilu
21	519.5	19.2	434	11	P81139	P81139 cavia porce
22	514	19.0	456	11	P97535	P97535 rattus norv
23	512	18.9	451	11	Q9QUN4	Q9qun4 rattus norv
24	494	18.2	456	11	Q99J51	Q99j51 mus musculu
25	489.5	18.1	452	6	Q95KP4	Q95kp4 equus cabal
26	489	18.1	456	11	Q8VI78	Q8vi78 mus musculu
27	487	18.0	451	4	Q8WWY8	Q8wwy8 homo sapien
28	477	17.6	451	11	Q8CIV3	Q8civ3 mus musculu
29	473	17.5	449	11	Q8BXB5	Q8bxb5 mus musculu
30	467	17.2	376	4	Q9UPD2	Q9upd2 homo sapien
31	467	17.2	456	4	O95991	O95991 homo sapien
32	466	17.2	440	4	Q86WX6	Q86wx6 homo sapien
33	458.5	16.9	452	6	Q9BDJ4	Q9bdj4 oryctolagus
34	450	16.6	347	13	Q7SZ70	Q7sz70 xenopus lae
35	437.5	16.1	540	5	Q9W448	Q9w448 drosophila
36	434	16.0	952	5	Q9VX01	Q9vx01 drosophila
37	431.5	15.9	427	6	Q28287	Q28287 canis famil
38	384.5	14.2	323	4	Q8TEC7	Q8tec7 homo sapien
39	384	14.2	421	11	Q8CI45	Q8ci45 mus musculu
40	382	14.1	394	5	Q9V7V4	Q9v7v4 drosophila
41	371	13.7	341	5	Q9VB89	Q9vb89 drosophila
42	367	13.5	284	13	Q7ZYK0	Q7zyk0 xenopus lae
43	364	13.4	341	5	Q9VB88	Q9vb88 drosophila
44	357	13.2	294	5	Q8MY66	Q8my66 bombyx mori
45	350.5	12.9	676	5	Q9VB94	Q9vb94 drosophila

ALIGNMENTS

RESULT 1

Q803Y3

ID Q803Y3 PRELIMINARY; PRT; 500 AA.

AC Q803Y3;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Similar to lipase, endothelial.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

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OM protein - protein search, using sw model

Run on: April 30, 2004, 08:03:37 ; Search time 20 Seconds
(without alignments)
2404.788 Million cell updates/sec

Title: US-09-277-401A-8
Perfect score: 2709
Sequence: 1 MSNSVPLLCFWSLCYCFAAG.....RKCRDGWRMKNETSPTVELP 500
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1227.5	45.3	490	1	S04331	lipoprotein lipase
2	1164	43.0	450	1	A27053	lipoprotein lipase
3	1164	43.0	475	2	JC4242	lipoprotein lipase
4	1164	43.0	478	2	S29846	lipoprotein lipase
5	1161	42.9	475	1	LIHUL	lipoprotein lipase
6	1160	42.8	474	1	JH0790	lipoprotein lipase
7	1159	42.8	474	1	A40570	lipoprotein lipase
8	1148	42.4	478	2	S18158	lipoprotein lipase
9	1140	42.1	465	1	A27330	lipoprotein lipase
10	1095.5	40.4	510	2	S15893	triacylglycerol li
11	1065	39.3	499	2	A28997	triacylglycerol li
12	1050.5	38.8	494	2	A27442	triacylglycerol li
13	574	21.2	457	2	I48206	triacylglycerol li
14	547.5	20.2	465	2	C43357	triacylglycerol li
15	544	20.1	470	2	A54232	lipase, CoPL-RP2 -
16	537	19.8	465	1	JC1318	triacylglycerol li
17	537	19.8	467	2	A43357	pancreatic lipase-
18	536	19.8	461	2	S21223	triacylglycerol li
19	534	19.7	473	2	S20612	triacylglycerol li
20	531	19.6	469	2	B43357	pancreatic lipase-

21	528.5	19.5	482	1	A46696	triacylglycerol li
22	522	19.3	465	2	S41084	triacylglycerol li
23	519.5	19.2	434	1	A49488	triacylglycerol li
24	514.5	19.0	482	1	A34671	triacylglycerol li
25	506.5	18.7	467	1	LIDG	triacylglycerol li
26	502	18.5	449	1	LIPG	triacylglycerol li
27	348.5	12.9	317	2	S32406	phospholipase A1 -
28	317.5	11.7	303	2	A44563	phospholipase A1 (
29	315.5	11.6	300	2	A44564	phospholipase A1 (
30	182	6.7	420	2	A25876	vitellogenin III p
31	166	6.1	439	1	VJFF1	vitellogenin I pre
32	165.5	6.1	172	2	A45658	triacylglycerol li
33	162.5	6.0	356	2	S49011	yolk protein 2 - b
34	161	5.9	437	2	S22889	vitellogenin 1 - M
35	155.5	5.7	422	2	S49012	yolk protein 3 - b
36	134.5	5.0	442	1	VJFF2	vitellogenin II pr
37	131	4.8	422	2	S22888	vitellogenin 2 - M
38	120	4.4	319	2	C96533	hypothetical prote
39	115	4.2	1078	2	S77162	DNA topoisomerase
40	106.5	3.9	1008	2	T49470	phosphatidic acid-
41	103	3.8	1289	2	C70044	probable phosphoes
42	98	3.6	6359	2	T31679	bacitracin synthet
43	96.5	3.6	303	2	S33490	hypothetical 303aa
44	95	3.5	553	2	B72863	HE65 protein - Aut
45	95	3.5	764	2	T25012	hypothetical prote

ALIGNMENTS

RESULT 1

S04331

lipoprotein lipase (EC 3.1.1.34) precursor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Mar-2000

C;Accession: S04331; A39093; S20598

R;Cooper, D.A.; Stein, J.C.; Strielemann, P.J.; Bensadoun, A.

Biochim. Biophys. Acta 1008, 92-101, 1989

A;Title: Avian adipose lipoprotein lipase: cDNA sequence and reciprocal regulation of mRNA levels in adipose and heart.

A;Reference number: S04331; MUID:89247453; PMID:2719965

A;Accession: S04331

A;Molecule type: mRNA

A;Residues: 1-490 <COO>

A;Cross-references: EMBL:X14670; NID:g63573; PIDN:CAA32800.1; PID:g63574

A;Note: part of this sequence, including the amino end of the mature protein, was confirmed by protein sequencing

A;Note: it is uncertain whether Met-1 or Met-7 is the initiator

R;Hoogewerf, A.J.; Bensadoun, A.

J. Biol. Chem. 266, 1048-1057, 1991

A;Title: Occurrence of sulfate in an asparagine-linked complex oligosaccharide of chicken adipose lipoprotein lipase.

A;Reference number: A39093; MUID:91093211; PMID:1985932

A;Accession: A39093

A;Molecule type: protein

A;Residues: 45-53, 'X', 55-66, 'Q', 68-69 <HOO>

A;Note: sulfate was shown to be incorporated on a GlcNAc residue of a complex oligosaccharide at Asn-70; the other two N-linked glycosylation sites do not contain sulfate

R;Cooper, D.A.; Lu, S.C.; Viswanath, R.; Freiman, R.N.; Bensadoun, A.

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OM protein - protein search, using sw model

Run on: April 30, 2004, 08:02:31 ; Search time 17 Seconds
(without alignments)
1531.475 Million cell updates/sec

Title: US-09-277-401A-8
Perfect score: 2709
Sequence: 1 MSNSVPLLCFWSLCYCFAAG.....RKCRDGWRMKNETSPTVELP 500
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : **SwissProt_42:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2709	100.0	500	1	LIPE_HUMAN	Q9y5x9 homo sapien
2	2207	81.5	500	1	LIPE_MOUSE	Q9wvg5 mus musculu
3	1227.5	45.3	490	1	LIPL_CHICK	P11602 gallus gall
4	1164	43.0	465	1	LIPL_BOVIN	P11151 bos taurus
5	1164	43.0	475	1	LIPL_PAPAN	P49060 papio anubi
6	1164	43.0	478	1	LIPL_SHEEP	Q29524 ovis aries
7	1161	42.9	474	1	LIPL_MOUSE	P11152 mus musculu
8	1161	42.9	475	1	LIPL_HUMAN	P06858 homo sapien
9	1160	42.8	474	1	LIPL_RAT	Q06000 rattus norv
10	1158	42.7	475	1	LIPL_MUSVI	O46647 mustela vis
11	1156	42.7	478	1	LIPL_FELCA	P55031 felis silve
12	1148	42.4	478	1	LIPL_PIG	P49923 sus scrofa
13	1140	42.1	465	1	LIPL_CAVPO	P11153 cavia porce
14	1088.5	40.2	510	1	LIPH_MOUSE	P27656 mus musculu
15	1067	39.4	499	1	LIPH_HUMAN	P11150 homo sapien
16	1045.5	38.6	494	1	LIPH_RAT	P07867 rattus norv
17	574	21.2	457	1	LIPP_MYOCO	Q64425 myocastor c
18	547.5	20.2	465	1	LIPP_HUMAN	P16233 homo sapien
19	544	20.1	470	1	LIP2_MYOCO	Q64424 myocastor c
20	537	19.8	467	1	LIP1_HUMAN	P54315 homo sapien
21	536	19.8	461	1	LIPP_HORSE	P29183 equus cabal
22	534	19.7	473	1	LIP1_RAT	P54316 rattus norv
23	533	19.7	465	1	LIPP_RABIT	Q02157 oryctolagus

24	531	19.6	469	1	LIP2_HUMAN	P54317	homo sapien
25	525	19.4	468	1	LIP2_RAT	P54318	rattus norv
26	522	19.3	465	1	LIPP_CAVPO	P50903	cavia porce
27	510.5	18.8	467	1	LIP1_CANFA	P06857	canis famil
28	509	18.8	465	1	LIPP_RAT	P27657	rattus norv
29	506.5	18.7	450	1	LIPP_PIG	P00591	sus scrofa
30	483	17.8	468	1	LIP2_MOUSE	P17892	mus musculu
31	394	14.5	80	1	LIPE_RAT	Q8vbx1	rattus norv
32	348.5	12.9	317	1	PA11_DOLMA	Q06478	dolichovesp
33	328.5	12.1	336	1	PA1_VESVU	P49369	vespula vul
34	317.5	11.7	303	1	PA12_DOLMA	P53357	dolichovesp
35	315.5	11.6	300	1	PA1_VESMC	P51528	vespula mac
36	310.5	11.5	301	1	PA1_POLAN	Q9u6w0	polistes an
37	182	6.7	420	1	VIT3_DROME	P06607	drosophila
38	166	6.1	439	1	VIT1_DROME	P02843	drosophila
39	161	5.9	437	1	VIT1_CERCA	P27878	ceratitidis c
40	134.5	5.0	442	1	VIT2_DROME	P02844	drosophila
41	131	4.8	422	1	VIT2_CERCA	P27587	ceratitidis c
42	118.5	4.4	761	1	AD24_MOUSE	Q9r160	mus musculu
43	115	4.2	1078	1	GYRB_SYNY3	P77966	synechocyst
44	108	4.0	2253	1	PKDR_HUMAN	Q9ntg1	homo sapien
45	102.5	3.8	2849	1	P1L1_HUMAN	Q8tdx9	homo sapien

ALIGNMENTS

RESULT 1

LIPE_HUMAN

ID LIPE_HUMAN STANDARD; PRT; 500 AA.
AC Q9Y5X9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Endothelial lipase precursor (EC 3.1.1.3) (Endothelial cell-derived
DE lipase) (EDL) (EL).
GN LIPG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=99253977; PubMed=10318835;
RA Hirata K.-I., Dichek H.L., Cioffi J.A., Choi S.Y., Leeper N.J.,
RA Quintana L., Kronmal G.S., Cooper A.D., Quertermous T.;
RT "Cloning of a unique lipase from endothelial cells extends the lipase
RT gene family.";
RL J. Biol. Chem. 274:14170-14175(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=99206614; PubMed=10192396;
RA Jaye M., Lynch K.J., Krawiec J., Marchadier D., Maugeais C., Doan K.,
RA South V., Amin D., Perrone M., Rader D.J.;
RT "A novel endothelial-derived lipase that modulates HDL metabolism.";
RL Nat. Genet. 21:424-428(1999).
RN [3]

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OM protein - protein search, using sw model.

Run on: April 30, 2004, 08:04:37 ; Search time 22 Seconds
(without alignments)
1173.318 Million cell updates/sec

Title: US-09-277-401A-8
Perfect score: 2709
Sequence: 1 MSNSVPLLCLFWSLCYCFAAG.....RKCRDGWRMKNETSPTVELP 500
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : **Issued Patents_AA:***
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2709	100.0	500	4	US-08-985-492-8	Sequence 8, Appli
2	1872	69.1	345	4	US-08-985-492-10	Sequence 10, Appl
3	1872	69.1	353	4	US-08-985-492-4	Sequence 4, Appli
4	1872	69.1	354	4	US-08-985-492-6	Sequence 6, Appli
5	1128.5	41.7	472	4	US-08-985-492-13	Sequence 13, Appl
6	1067	39.4	499	4	US-08-985-492-14	Sequence 14, Appl
7	555	20.5	473	4	US-09-411-132A-7	Sequence 7, Appli
8	547.5	20.2	465	4	US-08-985-492-15	Sequence 15, Appl
9	547.5	20.2	465	4	US-09-411-132A-6	Sequence 6, Appli
10	537	19.8	467	4	US-09-411-132A-4	Sequence 4, Appli
11	534	19.7	473	4	US-09-411-132A-8	Sequence 8, Appli
12	531	19.6	469	4	US-09-411-132A-5	Sequence 5, Appli
13	518.5	19.1	467	4	US-09-411-132A-3	Sequence 3, Appli
14	510.5	18.8	467	4	US-09-411-132A-10	Sequence 10, Appl
15	506.5	18.7	467	4	US-09-411-132A-9	Sequence 9, Appli
16	419.5	15.5	125	1	US-08-180-209B-20	Sequence 20, Appl
17	419.5	15.5	125	1	US-08-385-745-20	Sequence 20, Appl

18	419.5	15.5	125	3	US-08-485-388-20	Sequence 20, Appl
19	419.5	15.5	125	3	US-08-474-853-20	Sequence 20, Appl
20	419.5	15.5	125	4	US-09-166-205B-20	Sequence 20, Appl
21	419.5	15.5	125	5	PCT-US94-02629-20	Sequence 20, Appl
22	416.5	15.4	123	1	US-08-180-209B-19	Sequence 19, Appl
23	416.5	15.4	123	1	US-08-385-745-19	Sequence 19, Appl
24	416.5	15.4	123	3	US-08-485-388-19	Sequence 19, Appl
25	416.5	15.4	123	3	US-08-474-853-19	Sequence 19, Appl
26	416.5	15.4	123	4	US-09-166-205B-19	Sequence 19, Appl
27	416.5	15.4	123	5	PCT-US94-02629-19	Sequence 19, Appl
28	415.5	15.3	123	1	US-08-180-209B-18	Sequence 18, Appl
29	415.5	15.3	123	1	US-08-385-745-18	Sequence 18, Appl
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38	348.5	12.9	317	3	US-08-474-853-17	Sequence 17, Appl
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40	348.5	12.9	317	4	US-09-806-658-7	Sequence 7, Appli
41	348.5	12.9	317	5	PCT-US94-02629-17	Sequence 17, Appl
42	323.5	11.9	300	1	US-08-180-209B-27	Sequence 27, Appl
43	323.5	11.9	300	1	US-08-385-745-27	Sequence 27, Appl
44	323.5	11.9	300	3	US-08-485-388-27	Sequence 27, Appl
45	323.5	11.9	300	3	US-08-474-853-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1

US-08-985-492-8

; Sequence 8, Application US/08985492

; Patent No. **6395530**

; GENERAL INFORMATION:

; APPLICANT: Jaye, Michael C.

; APPLICANT: Doan, Kim-Anh T.

; APPLICANT: Krawiec, John A.

; APPLICANT: Lynch, Kevin J.

; APPLICANT: Amin, Dilip V.

; APPLICANT: South, Victoria J.

; TITLE OF INVENTION: LLG POLYPEPTIDES OF THE TRIACYLGLYCEROL

; TITLE OF INVENTION: LIPASE FAMILY, AND COMPOSITIONS AND METHODS FOR THEIR SE

; TITLE OF INVENTION: IN ENZYMATIC HYDROLYSIS, AND PROTEIN AND GENE THERAPIES

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Rd. 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
2771.896 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 1138120
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2709	100.0	500	14	US-10-128-449A-8	Sequence 8, Appli
3	2709	100.0	500	14	US-10-354-358-46	Sequence 46, Appl
4	2350	86.7	440	15	US-10-210-130-90	Sequence 90, Appl
5	1872	69.1	345	14	US-10-128-449A-10	Sequence 10, Appl
6	1872	69.1	353	14	US-10-128-449A-4	Sequence 4, Appli

7	1872	69.1	354	9	US-09-978-295A-178	Sequence 178, App
8	1872	69.1	354	9	US-09-978-697-178	Sequence 178, App
9	1872	69.1	354	9	US-09-978-192A-178	Sequence 178, App
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16	1872	69.1	354	10	US-09-978-564A-178	Sequence 178, App
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42	1872	69.1	354	12	US-10-144-993-400	Sequence 400, App
43	1872	69.1	354	12	US-10-158-787-400	Sequence 400, App
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ALIGNMENTS

RESULT 1

US-10-211-462-229

; Sequence 229, Application US/10211462

; Publication No. US20040033495A1

; GENERAL INFORMATION:

; APPLICANT: Murray, Richard

; APPLICANT: Glynne, Richard

; APPLICANT: Watson, Susan R.

; APPLICANT: Aziz, Natasha

; APPLICANT: Eos Biotechnology, Inc.

; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and

; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators

; FILE REFERENCE: 018501-006200US

; CURRENT APPLICATION NUMBER: US/10/211,462

; CURRENT FILING DATE: 2003-02-13

; PRIOR APPLICATION NUMBER: US 09/784,356

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OM protein - protein search, using sw model

Run on: April 30, 2004, 08:01:57 ; Search time 59 Seconds
(without alignments)
2394.470 Million cell updates/sec

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Perfect score: 2709
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
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3	2709	100.0	500	3	AAB19178	Aab19178 Human LIP
4	2709	100.0	500	5	AAO14635	Aao14635 Human lip
5	2709	100.0	500	6	ABU03569	Abu03569 Angiogene
6	2709	100.0	500	6	ABR64225	Abr64225 Angiogene
7	2709	100.0	500	7	ADE38385	Ade38385 Human pro
8	2350	86.7	440	7	ADE47728	Ade47728 Human NOV
9	2195	81.0	500	2	AAY23760	Aay23760 Mouse end
10	1872	69.1	345	2	AAW59793	Aaw59793 Amino aci
11	1872	69.1	345	3	AAB19179	Aab19179 The catal
12	1872	69.1	353	2	AAW59790	Aaw59790 Amino aci
13	1872	69.1	353	3	AAB19176	Aab19176 A partial
14	1872	69.1	354	2	AAW59791	Aaw59791 Amino aci
15	1872	69.1	354	2	AAY41711	Aay41711 Human PRO
16	1872	69.1	354	3	AAB44267	Aab44267 Human PRO

17	1872	69.1	354	3	AAB24413	Aab24413	Human	PRO
18	1872	69.1	354	3	AAB19177	Aab19177	Human	LIP
19	1872	69.1	354	4	AAU12371	Aau12371	Human	PRO
20	1872	69.1	354	4	AAB49892	Aab49892	Human	PRO
21	1872	69.1	354	4	AAB50912	Aab50912	Human	PRO
22	1872	69.1	354	6	ABO17815	Abo17815	Novel	hum
23	1872	69.1	354	6	ABO25213	Abo25213	Novel	hum
24	1872	69.1	354	6	ABU81069	Abu81069	Human	PRO
25	1872	69.1	354	6	ABU72219	Abu72219	Novel	hum
26	1872	69.1	354	6	ABU66769	Abu66769	Human	PRO
27	1872	69.1	354	6	ABU84899	Abu84899	Human	sec
28	1872	69.1	354	6	ABU59850	Abu59850	Novel	sec
29	1872	69.1	354	6	ABU61097	Abu61097	Human	PRO
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31	1872	69.1	354	6	ABU80366	Abu80366	Human	sec
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45	1872	69.1	354	6	ADA97088	Ada97088	Human	PRO

ALIGNMENTS

RESULT 1

AAW59792

ID AAW59792 standard; protein; 500 AA.

AC AAW59792;

DT 26-OCT-1998 (first entry)

DE Amino acid sequence of lipase like protein LLGXL.

KW Human lipase like gene; LLGXL; human lipoprotein lipase; hepatic lipase;

KW heparin; phosphatidylcholine ester; laundry detergent; serum lipid;

KW atherosclerosis; diabetes; hyperlipidemia; intrahepatic cholestasis.

OS Homo sapiens.

PN WO9824888-A2.

PD 11-JUN-1998.

PF 05-DEC-1997; 97WO-US022331.

PR 06-DEC-1996; 96US-0032254P.

PR 06-DEC-1996; 96US-0032783P.

PA (RHON) RHONE-POULENC RORER PHARM INC.

PI Jaye MC, Doan KT, Krawiec JA, Lynch KJ, Amin DV, South VJ;

DR WPI; 1998-333310/29.

DR N-PSDB; AAV41692.

PT Lipase like gene polypeptides - used for hydrolysis of

PT phosphatidylcholine esters or for treating e.g. atherosclerosis,

PT diabetes, hyperlipidemia or intrahepatic cholestasis.

PS Claim 3; Page 56-58; 94pp; English.

CC This is the amino acid sequence of the human lipase like protein (LLGXL).

CC It has homology with human lipoprotein lipase and hepatic lipase, and

CC binds to heparin. The LLGXL polypeptides can be used for the enzymatic